

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 11, 2005, 16:49:33 ; Search time 2179 seconds
(without alignments)
6079.103 Million cell updates/sec

Title: US-09-824-134-1_COPY_388_735
Perfect score: 348
Sequence: 1 TTTCGAGCGGGCGGGCGGC.....GGGCATGTCCCGCATGTCA 348

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_g881:*
9: gb_g882:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	348	100.0	719	2 BE275002	BE275002 601122536
2	348	100.0	774	2 BE275052	BE275052 601122604
3	348	100.0	850	5 BU957269	BU957269 AGENCOURT
4	348	100.0	931	5 BU535532	BU535532 AGENCOURT
5	348	100.0	940	5 BQ672502	BQ672502 AGENCOURT
6	348	100.0	947	5 BU197303	BU197303 AGENCOURT
7	348	100.0	965	1 AL548504	AL548504 AGENCOURT
8	348	100.0	993	1 AL527771	AL527771 AL527771
9	348	100.0	1029	9 AY401682	AY401682 Homo sapi
10	348	100.0	1134	1 AL544558	AL544558 AL544558
11	348	100.0	1595	3 CR595812	CR595812 full-leng
12	348	100.0	1595	3 CR615437	CR615437 full-leng
13	348	100.0	1614	3 CR621957	CR621957 full-leng
14	348	100.0	1618	3 CR591208	CR591208 full-leng
15	348	100.0	1629	3 CR616686	CR616686 full-leng
16	348	100.0	1634	3 CR608391	CR608391 full-leng
17	348	100.0	1650	3 CR596013	CR596013 full-leng
18	348	100.0	1653	3 CR593331	CR593331 full-leng
19	348	100.0	1653	3 CR607000	CR607000 full-leng
20	348	100.0	1663	3 CR593101	CR593101 full-leng
21	348	100.0	1689	3 BC025733	BC025733 Homo sapi
22	348	100.0	1691	3 CR600474	CR600474 full-leng
23	348	100.0	1702	3 CR610334	CR610334 full-leng
24	348	100.0	1721	3 CR599691	CR599691 full-leng

25	348	100.0	1806	3 CR605817	CR605817 full-leng
26	347.6	99.9	949	1 AL552532	AL552532 AL552532
27	346.8	99.7	1016	1 AL527192	AL527192 AL527192
28	346.8	99.7	1036	5 BX441966	BX441966 BX441966
29	346.4	99.5	806	4 B1465298	B1465298 603206617
30	345.2	99.2	1061	1 AL518571	AL518571 AL518571
31	344.8	99.1	614	2 AW245754	AW245754 2823021.5
32	344.8	99.1	937	2 BE784749	BE784749 601473661
33	344.4	99.0	870	5 BX448882	BX448882 BX448882
34	343.6	98.7	1035	1 AL557131	AL557131 AL557131
35	341	98.0	1099	5 BX354591	BX354591 BX354591
36	337	96.8	885	4 B1193429	B1193429 602947063
37	337	96.8	887	7 CF264787	CF264787 AGENCOURT
38	337	96.8	1084	2 BE794964	BE794964 601589730
39	336.6	96.7	1023	5 BX331772	BX331772 BX331772
40	336.6	96.7	1038	1 AL528496	AL528496 AL528496
41	336	96.6	754	2 BE563599	BE563599 601334715
42	336	96.6	870	2 BE888978	BE888978 601513909
43	335.8	96.5	1107	1 AL556073	AL556073 AL556073
44	335.4	96.4	859	4 BG751059	BG751059 602729849

ALIGNMENTS

RESULT 1
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LOCUS 601122536F1 NIH_MCC_20 Homo sapiens cDNA clone IMAGE:3346617 5',
DEFINITION mRNA sequence.
ACCESSION BE275002
VERSION BE275002.1 GI:9149952
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 719)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM136 row: h column: 10
High quality sequence stop: 717.
Location/Qualifiers
1. 719
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3346617"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 20"
/notes="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

FEATURES
source

Query Match 100.0%; Score 348; DB 2; Length 719;
Best Local Similarity 100.0%; Pred. No. 1.2e-83;

Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCAGAGGGGGGGCGCGCGCGCGCGCTGGGGAAGAACCTGTGTGACGATTT 60
 Db 136 TTTCAGAGGGGGGGCGCGCGCGCGCGCTGGGGAAGAACCTGTGTGACGATTT 195
 QY 61 AACGTATATGTGATAATTTGGGGAAGATTGGGGAAGGCTGGCTCGTCAAGATC 120
 Db 196 AACGTATATGTGATAATTTGGGGAAGATTGGGGAAGGCTGGCTCGTCAAGATC 255
 QY 121 TCAGACACCAAGATCGACAGATCGAGACAGATACCCCGCAACCTGACAGCGGTG 180
 Db 256 TCAGACACCAAGATCGACAGATCGAGACAGATACCCCGCAACCTGACAGCGGTG 315
 QY 181 CGGGAGTCACTGAGAACTCGAAGAACACAGAGAGGAGACGCAAGTGGCCCACTG 240
 Db 316 CGGGAGTCACTGAGAACTCGAAGAACACAGAGAGGAGACGCAAGTGGCCCACTG 375
 QY 241 GTGGGGGCTCTCAGTCTCGCAGATGAACCTGGTGGCTGACCTGGTACAGAGGTTTCA 300
 Db 376 GTGGGGGCTCTCAGTCTCGCAGATGAACCTGGTGGCTGACCTGGTACAGAGGTTTCA 435
 QY 301 CAGGCGCTGACCTCCAGAACAGAGTGGGGCCATGTCCCGCATGTCA 348
 Db 436 CAGGCGCTGACCTCCAGAACAGAGTGGGGCCATGTCCCGCATGTCA 483

RESULT 2
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 LOCUS 601122604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346608 5',
 DEFINITION mRNA sequence.
 BE275052
 BE275052.1 GI:9150002
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: ATCC/DCTD/DRP
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LCM136 row: h column: 01
 High quality sequence stop: 733.
 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3346608"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_20"
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

FEATURES
 source

1. 774
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3346608"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_20"
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 100.0%; Score 348; DB 2; Length 774;

Best Local Similarity 100.0%; Pred. No. 1.2e-83;
 Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCAGAGGGGGGGCGCGCGCGCGCGCTGGGGAAGAACCTGTGTGACGATTT 60
 Db 137 TTTCAGAGGGGGGGCGCGCGCGCGCGCTGGGGAAGAACCTGTGTGACGATTT 196
 QY 61 AACGTATATGTGATAATTTGGGGAAGATTGGGGAAGGCTGGCTCGTCAAGATC 120
 Db 197 AACGTATATGTGATAATTTGGGGAAGATTGGGGAAGGCTGGCTCGTCAAGATC 256
 QY 121 TCAGACACCAAGATCGACAGATCGAGACAGATACCCCGCAACCTGACAGCGGTG 180
 Db 257 TCAGACACCAAGATCGACAGATCGAGACAGATACCCCGCAACCTGACAGCGGTG 316
 QY 181 CGGGAGTCACTGAGAACTCGAAGAACACAGAGAGGAGACGCAAGTGGCCCACTG 240
 Db 317 CGGGAGTCACTGAGAACTCGAAGAACACAGAGAGGAGACGCAAGTGGCCCACTG 376
 QY 241 GTGGGGGCTCTCAGTCTCGCAGATGAACCTGGTGGCTGACCTGGTACAGAGGTTTCA 300
 Db 377 GTGGGGGCTCTCAGTCTCGCAGATGAACCTGGTGGCTGACCTGGTACAGAGGTTTCA 436
 QY 301 CAGGCGCTGACCTCCAGAACAGAGTGGGGCCATGTCCCGCATGTCA 348
 Db 437 CAGGCGCTGACCTCCAGAACAGAGTGGGGCCATGTCCCGCATGTCA 484

RESULT 3
 BU957269
 LOCUS AGENCOURT 10622000 NIH_MGC_107 Homo sapiens cDNA clone
 DEFINITION IMAGE:6731271 5', mRNA sequence.
 BU957269
 BU957269.1 GI:24186841
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LCM3057 row: g column: 14
 High quality sequence stop: 650.
 Location/Qualifiers
 1. 850
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6731271"
 /tissue_type="adenocarcinoma, cell line"
 /lab_host="NIH_MGC_107"
 /note="Organ: breast; Vector: pOTB7; Site 1: EcoRI;
 Site 2: XhoI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

FEATURES
 source

1. 850
 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /clone="IMAGE:6731271"
 /tissue_type="adenocarcinoma, cell line"
 /lab_host="NIH_MGC_107"
 /note="Organ: breast; Vector: pOTB7; Site 1: EcoRI;
 Site 2: XhoI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN

Note: this is a NIH MGC Library.

Query Match	100.0%;	Score 348;	DB 5;	Length 850;
Best Local Similarity	100.0%;	Pred. No. 1.2e-83;		
Matches 348;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
1	TTTCGAGGCGGGGCGCGCGCGGGCGCGCGCTCTGGGGAAGAAGACCTCTGTGTGCAGCAATTT	60		
92	TTTCGAGGCGGGGCGCGCGCGGGCGCGCGCTCTGGGGAAGAAGACCTCTGTGTGCAGCAATTT	151		
61	AACGTCATATGTGATAATCTGGGGGAAGAATTGGGAAGGCTGGCTGTCAGCTCAAAAGTC	120		
152	AACGTCATATGTGATAATCTGGGGGAAGAATTGGGAAGGCTGGCTGTCAGCTCAAAAGTC	211		
121	TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCGGCACTCGACAGAGCGGTGTG	180		
212	TCAGACACCAAGATCGACAGCATCGAGGACAGATACCCCGGCACTCGACAGAGCGGTGTG	271		
181	CGGGAGTCACTGAGATCTGGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACTGTG	240		
272	CGGGAGTCACTGAGATCTGGGAAGAACACAGAGAAGGAGAACGCAACAGTGGCCCACTGTG	331		
241	GTGGGGGCTCTCAGGTCCTCCAGATGAACCTGTGTGGCTTGACCTGGTCAAGAGAGTTTCAG	300		
332	GTGGGGGCTCTCAGGTCCTCCAGATGAACCTGTGTGGCTTGACCTGGTCAAGAGAGTTTCAG	391		
301	CAGGCCCGGTGAACCTCCAGAACAGGAGTGGGGCCATGTGTCCCGATGTCA	348		
392	CAGGCCCGGTGAACCTCCAGAACAGGAGTGGGGCCATGTGTCCCGATGTCA	439		

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FEATURES
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                /mol_type="mRNA"
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                /notes="Organ: breast; Vector: pOTB7; Site_1: EcoRI;
                Site_2: XhoI; cDNA made by oligo-dT priming.
                Directionally cloned into EcoRI/XhoI sites using the
                following 5' adaptor: GGCACGAG(G). Library constructed by
                Ling Hong in the laboratory of Gerald M. Rubin (University
                of California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies)."

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ORIGIN

Query Match	100.0%;	Score	348;	DB	5;	Length	331;		
Best Local Similarity	100.0%;	Pred. No.	1.3e-83;						
Matches	348;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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92	TTTCGAGGCGGGCGCGCGCGCGCGCGCTCTGGGGAAGAAGACTGTGTGTCAGCATTT	151							
61	AACGTCATATGTGATAATGTGGGGAAGAATTGGAGAAGCTCGCTCGTCAGCTCAAAATC	120							
152	AACGTCATATGTGATAATGTGGGGAAGAATTGGAGAAGCTCGCTCGTCAGCTCAAAATC	211							
121	TCAGACACCAAGATTCGACGATTCGAGGACAGATACCCCGCAACCTGACAGAGCGGTG	180							
212	TCAGACACCAAGATTCGACGATTCGAGGACAGATACCCCGCAACCTGACAGAGCGGTG	271							
181	CGGGAGTCACTCAGGAATCTGGGAAGAACACAGAGAAGGAGAACCGCAACAGTGCACCCTG	240							
272	CGGGAGTCACTCAGGAATCTGGGAAGAACACAGAGAAGGAGAACCGCAACAGTGCACCCTG	331							
241	GTGGGGGCTCTCAGGTCTCTCCAGATGAACCTGTGTGGCTGACCTCGTCAAGAGAGTTTCAG	300							
332	GTGGGGGCTCTCAGGTCTCTCCAGATGAACCTGTGTGGCTGACCTCGTCAAGAGAGTTTCAG	391							
301	CAGGCCCGGTGAACCTCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA	348							
392	CAGGCCCGGTGAACCTCAGAACAGGAGTGGGGCCATGTCCCCGATGTCA	439							

RESULT 5

BQ672502	940 bp	mRNA	linear	EST 15-JUL-2002
ACCESSION	AGENCOUTR 8349344	NIH_MGC_102	Homo sapiens	cdna clone IMAGE:6276350
VERSION	5',	mRNA	sequence.	
KEYWORDS	BQ672502			
SOURCE	BQ672502.1	GI:21783336		
ORGANISM	EST.			
REFERENCE	Homo sapiens			
AUTHORS	Homo sapiens			
TITLE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
JOURNAL	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
COMMENT	1. (bases 1 to 940)			
	NIH-MGC http://mgc.nci.nih.gov/ .			
	National Institutes of Health, Mammalian Gene Collection (MGC)			
	Unpublished (1999)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgabs-r@mail.nih.gov			
	Tissue procurement: ATCC			
	cdna Library Preparation: Rubin Laboratory			
	cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
	DNA Sequencing by: Agencourt Bioscience Corporation			
	Clone distribution: MGC clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LLNL at:			
	http://image.llnl.gov			
	Plate: LLCM2460	row: p	column: 15	
	High quality sequence	row: p	column: 488.	

FEATURES
SOURCE

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/mol_type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:6276350"
/tissue_type="epidermoid carcinoma, cell line"
/lab host="DHI0B (phage-resistant)"
/clone lib="NIH MGC 102"
/notes="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M Rubin

```


Matches	348;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	TTTCAGGCGGGGGCGGCGGCGCGCGCCCTGTGGGGAAGAAGACCTGTGTGTCAGCAATTT	60						
Db	376	TTTCAGGCGGGGGCGGCGGCGCGCGCCCTGTGGGGAAGAAGACCTGTGTGTCAGCAATTT	435						
QY	61	AACGTCTATGTGTGTAATATGTGTGGGGAAGAAGATTGTGAGAAAGGCTGTGCTCTAGCTCAAAGTC	120						
Db	436	AACGTCTATATGTGTGTAATATGTGTGGGGAAGAAGATTGTGAGAAAGGCTGTGCTCTAGCTCAAAGTC	495						
QY	121	TCAGACACCAAGATTCGACAGCATCGAGGACAGATACCCCGCCACCTTCGACAGAGCGGTG	180						
Db	496	TCAGACACCAAGATTCGACAGCATCGAGGACAGATACCCCGCCACCTTCGACAGAGCGGTG	555						
QY	181	CGGAGTCACTTGAGAAATCTGGAGAAACACAGAGAGGAGAAACGCAACAGTGGCGCCACCTG	240						
Db	556	CGGAGTCACTTGAGAAATCTGGAGAAACACAGAGAGGAGAAACGCAACAGTGGCGCCACCTG	615						
QY	241	GTGGGGGCTCTCAGGTCCTCCAGATGAACCTGGTGGCTGCACTTGGTACAGAGGTTTCA	300						
Db	616	GTGGGGGCTCTCAGGTCCTCCAGATGAACCTGGTGGCTGCACTTGGTACAGAGGTTTCA	675						
QY	301	CAGGCCCGTGACCTTCCAGAACAGAGAGTGGGGCCATGTCCCCGATGTCA	348						
Db	676	CAGGCCCGTGACCTTCCAGAACAGAGAGTGGGGCCATGTCCCCGATGTCA	723						

RESULT 12	CR615437	1595 bp	mRNA	linear	HTC 21-JUL-2004
LOCUS	CR615437				
DEFINITION	full-length cDNA clone CSQD0005YM20 of Hela cells Cot 25-normalized of Homo sapiens (human).				
ACCESSION	CR615437				
VERSION	CR615437.1	GI:50496244			
KEYWORDS	HTC; CNSLT CDNA.				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished				
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue 2 (bases 1 to 1595)				
REFERENCE	2 (bases 1 to 1595)				

TITLE	Direct Submission
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES	source	Location/Qualifiers
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		/mol_type="mRNA"
		/db_xref="taxon:9606"
		/clone="C90DK005YM20"
		/tissue_type="Hela cells Cot 25-normalized"
		/plasmid="pCMVSPORT 6"

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Query Match      100.0%; Score 348; DB 3; Length 1595;
Best Local Similarity 100.0%; Pred. No. 1.4e-83;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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328	TTCAGGCGGGCGGCCCGGGCCGCCTGGGGGAAGACCTGTGTGCAGCATTT	387
61	AACGTCATATGTGATAAATTGTGGGAAAGAATTGAGAAAGCTGTGCTCGTCAAGTC	120
388	AACGTCATATGTGATAAATTGTGGGAAAGAATTGAGAAAGCTGTGCTCGTCAAGTC	447
121	TCAGACACCAGAATCGACAGCATCGAGGACAGATACCCCGCAAACCTGCACAGAGCGTG	180
448	TCAGACACCAGAATCGACAGCATCGAGGACAGATACCCCGCAAACCTGCACAGAGCGTG	507
181	CGGGAGTCACTGAGAAATCTGGAAGAACACAGAGAAAGAGAACCGCAACAGTGGGCCACTG	240
508	CGGGAGTCACTGAGAAATCTGGAAGAACACAGAGAAAGAGAACCGCAACAGTGGGCCACTG	567
241	GTTGGGGCTCTCAGGTCCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTTCA	300
568	GTTGGGGCTCTCAGGTCCCTGCCAGATGAACCTGGTGGCTGACCTGGTACAAGAGGTTTCA	627
301	CAGGGCCGCTGACCTCCAGAACAGGAGTGGGGCCATGTCCCAGATGTCA	348
628	CAGGCCGCTGACCTCCAGAACAGGAGTGGGGCCATGTCCCAGATGTCA	675

RESULT 13	
CR6211957	
LOCUS	1614 bp mRNA linear HTC 21-JUL-2004
DEFINITION	full-length cDNA clone CS0DI067YD16 of Placenta Cot 25-normalized of Homo sapiens (human).
ACCESSION	CR6211957
VERSION	CR6211957.1 GI:50502764
KEYWORDS	HTC; CNSLT CDNA.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 1614)
TITLE	Li, W. B., Gruber, C., Jesse, J., and Polayes, D.
JOURNAL	Full-length cDNA libraries and normalized
REMARK	Unpublished Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Paradise Avenue 2 (bases 1 to 1614)
REFERENCE	Genoscope.
AUTHORS	Direct Submission
TITLE	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage
JOURNAL	BP 191 91006 EVRY cedex - FRANCE (E-mail : secref@genoscope.cns.fr) Web : www.genoscope.cns.fr

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FEATURES
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Qy	61 AACGTCATATGTGATAATGTGGGAAAGATTGGAGAGGCTGGCTCAGCTCAAGTGC	120	

Db 556 CGGGAGTCACTGAGAAATCTGAAGAAACACAGAGAGAGAGACGCAACAGTGGCCCCACCTG 615
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